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TECH CENTER 1600/2900

1600

**RAW SEQUENCE LISTING**

PATENT APPLICATION: US/09/875,321A

DATE: 02/03/2003

TIME: 09:15:39

Input Set : A:\Sequence listing.TXT  
 Output Set: N:\CRF4\02032003\I875321A.raw

4 <110> APPLICANT: Curtis, Rory A.J.  
 6 <120> TITLE OF INVENTION: 52906, 33408, AND 12189, NOVEL POTASSIUM  
 7 CHANNEL FAMILY MEMBERS AND USES THEREOF  
 10 <130> FILE REFERENCE: 10448-061001  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/875,321A  
 C--> 12 <141> CURRENT FILING DATE: 2000-06-06  
 12 <150> PRIOR APPLICATION NUMBER: US 60/209,845  
 13 <151> PRIOR FILING DATE: 2000-06-06  
 15 <160> NUMBER OF SEQ ID NOS: 13  
 17 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 3525  
 21 <212> TYPE: DNA  
 22 <213> ORGANISM: Homo sapiens  
 24 <220> FEATURE:  
 25 <221> NAME/KEY: CDS  
 26 <222> LOCATION: (638)...(3178)  
 28 <400> SEQUENCE: 1  
 29 gcgtccgcag attccagagc ctgccggctg ggaaagatcc ggtctcgaaaa tcggctatga 60  
 30 tcccgcagcg gccaaggcgag ggctcaggcc ccgggattct cccccacacgc tgctgcactg 120  
 31 ggcgcagccgg tcgccaaact ttttctcccc aaagccagtgc ccccccgcagt tacttggcg 180  
 32 gcagccggca gcccactctc ggcgggatgatc tctggagaa gccccgcgtgg gacgaggggg 240  
 33 ctgctgtttt gcagccctgc gaggcgtgca gtcggagaag tggtcgggggt tccacaccgt 300  
 34 ccctgagcct gccccctggc caaggtggcc cgacgtgctg cagtggctgg cgccgggtgat 360  
 35 ccgggcagcg cgtccggcac tagtcaaggg ggcagccggca cgggagggag gggcccttt 420  
 36 ctctttctc ctcccccctgc agcccagctg cactgcgtgg gggctctcca tctccacgca 480  
 37 atcagcaggc ggaatccctg ccctggagcg ccctggctct ggactgcacc ccccttagggt 540  
 38 ttgtcctgca gattcttc cccatcttc tctgccacac acgcttcctt aagccgcgcg 600  
 39 cccgccaaac tcagtctcggtcccccgcagg tgatgtc atg ccc att gtt ttg gtg 655  
 40 Met Pro Ile Val Leu Val  
 41 1 5  
 43 cgc cca acc aat cgg act cgc cgc ctg gat tct acc gga gcc ggc atg 703  
 44 Arg Pro Thr Asn Arg Thr Arg Arg Leu Asp Ser Thr Gly Ala Gly Met  
 45 10 15 20  
 47 ggc cct tcc tcg cac cag cag cag gag tcc ccg ctc ccg acc ata acg 751  
 48 Gly Pro Ser Ser His Gln Gln Glu Ser Pro Leu Pro Thr Ile Thr  
 49 25 30 35  
 51 cat tgc gca ggg tgc acc acc gct tgg tct ccc tgc agc ttt aac acg 799  
 52 His Cys Ala Gly Cys Thr Ala Trp Ser Pro Cys Ser Phe Asn Ser  
 53 40 45 50  
 55 cct gac atg gaa acc cca ttg cag ttc cag cgc ggc ttc ttc cca gag 847  
 56 Pro Asp Met Glu Thr Pro Leu Gln Phe Gln Arg Gly Phe Phe Pro Glu  
 57 55 60 65 70

**ENTERED**

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59 cag ccg ccg ccg ccg ccg tcc tca cac ctg cat tgc cag cag cag	895
60 Gln Pro Pro Pro Pro Arg Ser Ser His Leu His Cys Gln Gln Gln	
61 75 80 85	
63 caa cag agc cag gac aag ccg tgc ccg ccc ttc gcg ccc ctc ccg cac	943
64 Gln Gln Ser Gln Asp Lys Pro Cys Pro Pro Phe Ala Pro Leu Pro His	
65 90 95 100	
67 cct cac cac cac ccg cac ctc gcg cac cag ccg gcc agc ggc ggc	991
68 Pro His His Pro His Leu Ala His Gln Gln Pro Ala Ser Gly Gly	
69 105 110 115	
71 agc agc cca tgc ctc cg <sup>g</sup> tgc aac agc tgc gcc tcc tcc ggt gcc ccg	1039
72 Ser Ser Pro Cys Leu Arg Cys Asn Ser Cys Ala Ser Ser Gly Ala Pro	
73 120 125 130	
75 gcg gcg ggg gcg gga gat aac ctg tcc ctg ctg ctc ccg acc tcc tcg	1087
76 Ala Ala Gly Ala Gly Asp Asn Leu Ser Leu Leu Arg Thr Ser Ser	
77 135 140 145 150	
79 ccc ggc ggc gcc ttc cg <sup>g</sup> acc ccg acc tcc tcg ccg ctg tcg ggc tcg	1135
80 Pro Gly Gly Ala Phe Arg Thr Arg Thr Ser Ser Pro Leu Ser Gly Ser	
81 155 160 165	
83 tcc tgc tgc tgc tgc tcg tcg ccg ccg ggc agc cag ctc aat	1183
84 Ser Cys Cys Cys Cys Ser Ser Arg Arg Gly Ser Gln Leu Asn	
85 170 175 180	
87 gtg agc gag ctg acg ccg tcc agc cat gcc agt gcg ctc ccg cag cag	1231
88 Val Ser Glu Leu Thr Pro Ser Ser His Ala Ser Ala Leu Arg Gln Gln	
89 185 190 195	
91 tac gcg cag cag tcc gcg cag cag tcg gcg tcc gcc tcc cag tac cac	1279
92 Tyr Ala Gln Gln Ser Ala Gln Gln Ser Ala Ser Ala Ser Gln Tyr His	
93 200 205 210	
95 cag tgc cac agc ctg cag ccc gcc gcc agc ccc acg ggc agc ctc ggc	1327
96 Gln Cys His Ser Leu Gln Pro Ala Ala Ser Pro Thr Gly Ser Leu Gly	
97 215 220 225 230	
99 agt ctg ggc tcc ggg ccc ccg ctc tcg cac cac cac cac ccg cac	1375
100 Ser Leu Gly Ser Gly Pro Pro Leu Ser His His His His His Pro His	
101 235 240 245	
103 ccg gcg cac cac cag cac ccc cag gcg ccg ccg gag agc aac	1423
104 Pro Ala His His Gln His Gln Pro Gln Ala Arg Arg Glu Ser Asn	
105 250 255 260	
107 ccc ttc acc gaa ata gcc atg agc agc tgc agg tac aac ggg ggc gtc	1471
108 Pro Phe Thr Glu Ile Ala Met Ser Ser Cys Arg Tyr Asn Gly Gly Val	
109 265 270 275	
111 atg cg <sup>g</sup> ccg ctc agc aac ttg agc gcg tcc ccg ccg aac ctg cac gag	1519
112 Met Arg Pro Leu Ser Asn Leu Ser Ala Ser Arg Arg Asn Leu His Glu	
113 280 285 290	
115 atg gac tca gag gcg cag ccc ctg cag ccc ccc gcg tct gtc gga gga	1567
116 Met Asp Ser Glu Ala Gln Pro Leu Gln Pro Pro Ala Ser Val Gly Gly	
117 295 300 305 310	
119 ggt ggc ggc gcg tcc tcc ccg tct gca gcc gct gcc gcc gcc gct	1615
120 Gly Gly Gly Ala Ser Ser Pro Ser Ala Ala Ala Ala Ala Ala Ala	
121 315 320 325	
123 gtt tcg tcc tca gcc ccc gag atc gtg gtg tct aag ccc gag cac aac	1663

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124 Val Ser Ser Ser Ala Pro Glu Ile Val Val Ser Lys Pro Glu His Asn			
125 330	335	340	
127 aac tcc aac aac ctg gcg ctc tat gga acc ggc ggc gga ggc agc act		1711	
128 Asn Ser Asn Asn Leu Ala Leu Tyr Gly Thr Gly Gly Ser Thr			
129 345	350	355	
131 gga gga ggc ggc ggc ggt ggc ggg agc ggg cac ggc agc agc agt ggc		1759	
132 Gly Gly Gly Gly Gly Gly Ser Gly His Gly Ser Ser Ser Gly			
133 360	365	370	
135 acc aag tcc agc aaa aag aaa aac cag aac atc ggc tac aag ctg ggc		1807	
136 Thr Lys Ser Ser Lys Lys Asn Gln Asn Ile Gly Tyr Lys Leu Gly			
137 375	380	385	390
139 cac cgg cgc gcc ctg ttc gaa aag cgc aag cgg ctc agc gac tac gcg		1855	
140 His Arg Arg Ala Leu Phe Glu Lys Arg Lys Arg Leu Ser Asp Tyr Ala			
141 395	400	405	
143 ctc atc ttc ggc atg ttc ggc atc gtg gtc atg gtc atc gag acc gag		1903	
144 Leu Ile Phe Gly Met Phe Gly Ile Val Val Met Val Ile Glu Thr Glu			
145 410	415	420	
147 ctg tcg tgg ggc gcc tac gac aag gcg tcg ctg tat tcc tta gct ctg		1951	
148 Leu Ser Trp Gly Ala Tyr Asp Lys Ala Ser Leu Tyr Ser Leu Ala Leu			
149 425	430	435	
151 aaa tgc ctt atc agt ctc tcc acg atc atc ctg ctc ggt ctg atc atc		1999	
152 Lys Cys Leu Ile Ser Leu Ser Thr Ile Ile Leu Leu Gly Leu Ile Ile			
153 440	445	450	
155 gtg tac cac gcc agg gaa ata cag ttg ttc atg gtg gac aat gga gca		2047	
156 Val Tyr His Ala Arg Glu Ile Gln Leu Phe Met Val Asp Asn Gly Ala			
157 455	460	465	470
159 gat gac tgg aga ata gcc atg act tat gag cgt att ttc ttc atc tgc		2095	
160 Asp Asp Trp Arg Ile Ala Met Thr Tyr Glu Arg Ile Phe Phe Ile Cys			
161 475	480	485	
163 ttg gaa ata ctg gtg tgt gct att cat ccc ata cct ggg aat tat aca		2143	
164 Leu Glu Ile Leu Val Cys Ala Ile His Pro Ile Pro Gly Asn Tyr Thr			
165 490	495	500	
167 ttc aca tgg acg gcc cgg ctt gcc ttc tcc tat gcc cca tcc aca acc		2191	
168 Phe Thr Trp Thr Ala Arg Leu Ala Phe Ser Tyr Ala Pro Ser Thr Thr			
169 505	510	515	
171 acc gct gat gtg gat att att tta tct ata cca atg ttc tta aga ctc		2239	
172 Thr Ala Asp Val Asp Ile Ile Leu Ser Ile Pro Met Phe Leu Arg Leu			
173 520	525	530	
175 tat ctg att gcc aga gtc atg ctt tta cat agc aaa ctt ttc act gat		2287	
176 Tyr Leu Ile Ala Arg Val Met Leu Leu His Ser Lys Leu Phe Thr Asp			
177 535	540	545	550
179 acc tcc tct aga agc att gga gca ctt aat aag ata aac ttc aat aca		2335	
180 Thr Ser Ser Arg Ser Ile Gly Ala Leu Asn Lys Ile Asn Phe Asn Thr			
181 555	560	565	
183 cgt ttt gtt atg aag act tta atg act ata tgc cca gga act gta ctc		2383	
184 Arg Phe Val Met Lys Thr Leu Met Thr Ile Cys Pro Gly Thr Val Leu			
185 570	575	580	
187 ttg gtt ttt agt atc tca tta tgg ata att gcc gca tgg act gtc cga		2431	
188 Leu Val Phe Ser Ile Ser Leu Trp Ile Ile Ala Ala Trp Thr Val Arg			

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189	585	590	595	
191	gct tgt gaa agg tac cat gat caa cag gat gtt act agc aac ttc ctt			2479
192	Ala Cys Glu Arg Tyr His Asp Gln Gln Asp Val Thr Ser Asn Phe Leu			
193	600	605	610	
195	gga gcg atg tgg ttg ata tca ata act ttt ctc tcc att ggt tat ggt			2527
196	Gly Ala Met Trp Leu Ile Ser Ile Thr Phe Leu Ser Ile Gly Tyr Gly			
197	615	620	625	630
199	gac atg gta cct aac aca tac tgt gga aaa gga gtc tgc tta ctt act			2575
200	Asp Met Val Pro Asn Thr Tyr Cys Gly Lys Gly Val Cys Leu Leu Thr			
201	635	640	645	
203	gga att atg ggt gct ggt tgc aca gcc ctg gtg gta gct gta gtg gca			2623
204	Gly Ile Met Gly Ala Gly Cys Thr Ala Leu Val Val Ala Val Val Ala			
205	650	655	660	
207	agg aag cta gaa ctt acc aaa gca gaa aaa cac gtg cac aat ttc atg			2671
208	Arg Lys Leu Glu Leu Thr Lys Ala Glu Lys His Val His Asn Phe Met			
209	665	670	675	
211	atg gat act cag ctg act aaa aga gta aaa aat gca gct gcc aat gta			2719
212	Met Asp Thr Gln Leu Thr Lys Arg Val Lys Asn Ala Ala Ala Asn Val			
213	680	685	690	
215	ctc agg gaa aca tgg cta att tac aaa aat aca aag cta gtg aaa aag			2767
216	Leu Arg Glu Thr Trp Leu Ile Tyr Lys Asn Thr Lys Leu Val Lys Lys			
217	695	700	705	710
219	ata gat cat gca aaa gta aga aaa cat caa cga aaa ttc ctg caa gct			2815
220	Ile Asp His Ala Lys Val Arg Lys His Gln Arg Lys Phe Leu Gln Ala			
221	715	720	725	
223	att cat caa tta aga agt gta aaa atg gag cag agg aaa ctg aat gac			2863
224	Ile His Gln Leu Arg Ser Val Lys Met Glu Gln Arg Lys Leu Asn Asp			
225	730	735	740	
227	caa gca aac act ttg gtg gac ttg gca aag acc cag aac atc atc tat			2911
228	Gln Ala Asn Thr Leu Val Asp Leu Ala Lys Thr Gln Asn Ile Met Tyr			
229	745	750	755	
231	gat atg att tct gac tta aac gaa agg agt gaa gac ttc gag aag agg			2959
232	Asp Met Ile Ser Asp Leu Asn Glu Arg Ser Glu Asp Phe Glu Lys Arg			
233	760	765	770	
235	att gtt acc ctg gaa aca aaa cta gag act ttg att ggt agc atc cac			3007
236	Ile Val Thr Leu Glu Thr Lys Leu Glu Thr Leu Ile Gly Ser Ile His			
237	775	780	785	790
239	gcc ctc cct ggg ctc ata agc cag acc atc agg cag cag cag aga gat			3055
240	Ala Leu Pro Gly Leu Ile Ser Gln Thr Ile Arg Gln Gln Gln Arg Asp			
241	795	800	805	
243	tcc att gag gct cag atg gag agc tac gac aag cac gtc act tac aat			3103
244	Phe Ile Glu Ala Gln Met Glu Ser Tyr Asp Lys His Val Thr Tyr Asn			
245	810	815	820	
247	gct gag cggt tcc cggt tcc tcg tcc agg agg cggt cggt tcc tct tcc aca			3151
248	Ala Glu Arg Ser Arg Ser Ser Arg Arg Arg Arg Ser Ser Ser Thr			
249	825	830	835	
251	gca cca cca act tca tca gag agt agc tagaagagaa taagttacc			3198
252	Ala Pro Pro Thr Ser Ser Glu Ser Ser			
253	840	845		

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255	acaaaataag	acttttgcc	atcatatgtt	caatattta	gcttttattg	taaagccccct	3258
256	atggttctaa	tcagcgttat	ccgggttctg	atgtcagaat	cctggaaacc	tgaacactaa	3318
257	gttttaggcc	aaaatgagtg	aaaactctt	tttttcttt	cagatgcaca	ggaatgcac	3378
258	ctattattgc	tatatagatt	gttcctctg	taatttcaact	aacttttat	tcatgcactt	3438
259	caaacaaaact	ttactactac	attatatgat	atataataaa	aaaagttaat	ttctgcaaaa	3498
260	aaaaaaaaaa	aaaaaaaaac	ggacggg				3525
262	<210>	SEQ ID NO:	2				
263	<211>	LENGTH:	847				
264	<212>	TYPE:	PRT				
265	<213>	ORGANISM:	Homo sapiens				
267	<400>	SEQUENCE:	2				
268	Met Pro Ile Val Leu Val Arg Pro Thr Asn Arg Thr Arg Arg	Leu Asp					
269	1 5 10 15						
270	Ser Thr Gly Ala Gly Met Gly Pro Ser Ser His Gln Gln Gln Glu Ser						
271	20 25 30						
272	Pro Leu Pro Thr Ile Thr His Cys Ala Gly Cys Thr Thr Ala Trp Ser						
273	35 40 45						
274	Pro Cys Ser Phe Asn Ser Pro Asp Met Glu Thr Pro Leu Gln Phe Gln						
275	50 55 60						
276	Arg Gly Phe Phe Pro Glu Gln Pro Pro Pro Pro Arg Ser Ser His						
277	65 70 75 80						
278	Leu His Cys Gln Gln Gln Gln Ser Gln Asp Lys Pro Cys Pro Pro						
279	85 90 95						
280	Phe Ala Pro Leu Pro His Pro His His Pro His Leu Ala His Gln						
281	100 105 110						
282	Gln Pro Ala Ser Gly Gly Ser Ser Pro Cys Leu Arg Cys Asn Ser Cys						
283	115 120 125						
284	Ala Ser Ser Gly Ala Pro Ala Ala Gly Ala Gly Asp Asn Leu Ser Leu						
285	130 135 140						
286	Leu Leu Arg Thr Ser Ser Pro Gly Gly Ala Phe Arg Thr Arg Thr Ser						
287	145 150 155 160						
288	Ser Pro Leu Ser Gly Ser Ser Cys Cys Cys Cys Cys Ser Ser Arg						
289	165 170 175						
290	Arg Gly Ser Gln Leu Asn Val Ser Glu Leu Thr Pro Ser Ser His Ala						
291	180 185 190						
292	Ser Ala Leu Arg Gln Gln Tyr Ala Gln Gln Ser Ala Gln Gln Ser Ala						
293	195 200 205						
294	Ser Ala Ser Gln Tyr His Gln Cys His Ser Leu Gln Pro Ala Ala Ser						
295	210 215 220						
296	Pro Thr Gly Ser Leu Gly Ser Leu Gly Ser Gly Pro Pro Leu Ser His						
297	225 230 235 240						
298	His His His His Pro His Pro Ala His His Gln His His Gln Pro Gln						
299	245 250 255						
300	Ala Arg Arg Glu Ser Asn Pro Phe Thr Glu Ile Ala Met Ser Ser Cys						
301	260 265 270						
302	Arg Tyr Asn Gly Gly Val Met Arg Pro Leu Ser Asn Leu Ser Ala Ser						
303	275 280 285						
304	Arg Arg Asn Leu His Glu Met Asp Ser Glu Ala Gln Pro Leu Gln Pro						
305	290 295 300						

**VERIFICATION SUMMARY**  
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L:12 M:270 C: Current Application Number differs, Replaced Current Application No  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date